

Figur 1A
IL17RLP Nucleotide and Amino Acid Sequence

1	GCACGAGCGATGTCGCTCGTGCCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCC	60
1	<u>M S L V L L S L A A L C R S A V P</u>	17
61	CGAGAGCCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAA	120
18	<u>R E P T V Q C G S E T G P S P E W M L Q</u>	37
121	CATGATCTAATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTT	180
38	H D L I P G D L R D L R V E P V T T S V	57
181	GCAACAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGC	240
58	A T G D Y S I L M N <u>V S W V L R A D A S</u>	77
	<i>Domain I</i>	
241	ATCCGCTTGTGAAGGCCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCTTAC	300
78	<u>I R L L</u> K A T K I C V T G K S N F Q S Y	97
	<i>Domain I</i>	
301	AGCTGTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCCTCTGGTGGT	360
98	S C V R C N Y T E A F Q T Q T R P S <u>G G</u>	117
361	AAATGGACATTTTCCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGG	420
118	<u>K W T F</u> S Y I G F P V E L N T V Y F I G	137
421	GCCATAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTC	480
138	A H N I P N A N M N E D G P S M S V N F	157
481	ACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTGTCAAGCCCGA	540
158	T S P G C L D H I M K Y K K K <u>C V K A G</u>	177
	<i>Domain II</i>	
541	AGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGAATGAGGAGACAGTAGAAGTGAAC	600
178	<u>S L W D P N I T</u> A C K K N E E T V E V N	197
	<i>Domain II</i>	
601	TTCACAACCACCTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATC	660
198	F T T T P L G N R Y M A L I Q H S T I I	217
661	GGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATT	720
218	G F S <u>Q V F E P H Q</u> K K Q T R A S V V I	237
	<i>Domain III</i>	
721	CCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGT	780
238	P V T G D S E G A T V Q L T P Y F P T C	257

Figure 1B
IL17RLP Nucleotide and Amino Acid Sequence

781	GGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCCACAAACAGGCGTCCCT	840
258	G S <u>D C I R H K G T V</u> V L C P Q <u>T G V P</u>	277
	<i>Domain IV</i>	<i>Domain V</i>
841	TTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGTGTCT	900
278	<u>F P L</u> D N <u>N K S K P G G W L P L L L L S</u>	297
	<i>Domain V</i>	
901	CTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGG	960
298	L L V A T W V L V A G I Y L M W R H E R	317
961	ATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTT	1020
318	I K K T S F S T T T L <u>L P P I K V L V V</u>	337
	<i>Domain VI</i>	
1021	TACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAC	1080
338	<u>Y P S E I C F H H T I C Y F T E F L Q N</u>	357
	<i>Domain VI</i>	
1081	CATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGT	1140
358	H <u>C R S E V I L</u> E K W Q K K K <u>I A E M G</u>	377
	<i>Domain VII</i>	<i>Domain VIII</i>
1141	CCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTCC	1200
378	P V Q W L A T Q K K A A D K V V F L L S	397
1201	AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAG	1260
398	N D V N S V C D G T C G K S E G S P S E	417
1261	AACTCTCAAGACTCTTCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGAT	1320
418	N S Q D S S P C L	426
1321	TCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAA	1380
1381	TGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGA	1440
1441	ACTTCTCCATGTCAAGTAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGG	1500
1501	CTGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGWGACCTTAAAGGCTTCCATCCAC	1560
1561	CAATTACAGGGAACCGTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCC	1620
1621	TTAGTAATTAAACATTTTATACCAATAAAATTTTCAAATATTGCTAATAATGTAGCAT	1680

Figure 1C
IL17RLP Nucleotide and Amino Acid Sequence

1681 TAACTAACGATTGGAAACTACATTTACAACCTCAAAGCTGTTTTATACATAGAAATCAAT 1740
1741 TACAGTTTTAATTGAAAACATAACCATTTTGATAATGCAACAATAAAGCATCTTCAGCC 1800
1801 AAAAAAAAAAAAAAAAAA 1816

Percent Similarity: 49.879 Percent Identity: 28.571

x

mIL17R.aa

401 NSVCDGTCGKSEGPSSENSQDSSPC 425
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 454 OAKWKAILGWAEPVQLRCDHWKPA 478

Figure 3
IL17RLP Protein Analysis

